

SEQUENCE LISTING

<110> NG FONG POH, LISA
REN, EE CHEE

<120> METHODS AND COMPOUNDS FOR ALTERING THE LOAD OF
HEPATITIS VIRUS

<130> 033946-1401

<140> 10/583,068

<141> 2006-06-15

<150> PCT/SG04/00368

<151> 2004-11-12

<150> 60/529,632

<151> 2003-12-16

<160> 136

<170> PatentIn Ver. 3.3

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Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala	
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Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu	
35 40 45	
ctt cag agc aag aat gct ggg gca gtg att gga aaa gga ggc aag aat	192
Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn	
50 55 60	
att aag gct ctc cgt aca gac tac aat gcc agt gtt tca gtc cca gac	240
Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp	
65 70 75 80	
agc agt ggc ccc gag cgc ata ttg agt atc agt gct gat att gaa aca	288
Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr	
85 90 95	
att gga gaa att ctg aag aaa atc atc cct acc ttg gaa gag ggc ctg	336
Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu	
100 105 110	
cag ttg cca tca ccc act gca acc agc cag ctc ccg ctc gaa tct gat	384
Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp	
115 120 125	
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Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp	
130 135 140	
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Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile	
145 150 155 160	
ggg gtc aaa ggt gct aaa att aaa gaa ctt cga gag aac act caa acc	528
Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr	
165 170 175	
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Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val	
180 185 190	
gtt ctt att gga gga aaa ccc gat agg gtt gta gag tgc ata aag atc	624
Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile	
195 200 205	
atc ctt gat ctt ata tct gag tct ccc atc aaa gga cgt gca cag cct	672
Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro	
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Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr	
225 230 235 240	

atg atg ttt gat gac cgt cgc gga cgc cca gtg gga ttt ccc atg cgg	768
Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg	
245 250 255	
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Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro	
260 265 270	
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Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly	
275 280 285	
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Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala	
290 295 300	
cgg aat ctt cct ctt cct cca cca cca cca cct aga ggg gga gac ctc	960
Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu	
305 310 315 320	
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Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met	
325 330 335	
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Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp	
340 345 350	
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Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly	
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Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly	
370 375 380	
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Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly	
385 390 395 400	
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Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu	
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Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp	
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Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln	
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 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
 1 5 10 15
 Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
 20 25 30
 Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
 35 40 45
 Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
 50 55 60
 Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp
 65 70 75 80
 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
 85 90 95
 Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
 100 105 110
 Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
 115 120 125
 Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
 130 135 140
 Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
 145 150 155 160
 Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
 165 170 175
 Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
 180 185 190
 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
 195 200 205
 Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
 210 215 220
 Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
 225 230 235 240
 Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
 245 250 255
 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
 260 265 270

Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
 275 280 285

Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
 290 295 300

Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
 305 310 315 320

Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
 325 330 335

Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
 340 345 350

Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
 355 360 365

Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
 370 375 380

Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
 385 390 395 400

Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
 405 410 415

Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
 420 425 430

Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
 435 440 445

Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
 450 455 460

<210> 103
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1392)

<400> 103
 atg gaa act gaa cag cca gaa gaa acc ttc cct aac act gaa acc aat 48
 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
 1 5 10 15

ggt gaa ttt ggt aaa cgc cct gca gaa gat atg gaa gag gaa caa gca 96
 Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
 20 25 30

ttt aaa aga tct aga aac act gat gag atg gtt gaa tta cgc att ctg	144
Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu	
35 40 45	
ctt cag agc aag aat gct ggg gca gtg att gga aaa gga ggc aag aat	192
Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn	
50 55 60	
att aag gct ctc cgt aca gac tac aat gcc agt gtt tca gtc cca gac	240
Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp	
65 70 75 80	
agc agt ggc ccc gag cgc ata ttg agt atc agt gct gat att gaa aca	288
Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr	
85 90 95	
att gga gaa att ctg aag aaa atc atc cct acc ttg gaa gag ggc ctg	336
Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu	
100 105 110	
cag ttg cca tca ccc act gca acc agc cag ctc ccg ctc gaa tct gat	384
Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp	
115 120 125	
gct gtg gaa tgc tta aat tac caa cac tat aaa gga agt gac ttt gac	432
Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp	
130 135 140	
tgc gag ttg agg ctg ttg att cat cag agt cta gca gga gga att att	480
Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile	
145 150 155 160	
ggg gtc aaa ggt gct aaa att aaa gaa ctt cga gag aac act caa acc	528
Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr	
165 170 175	
acc atc aag ctt ttc cag gaa tgc tgt cct cat tcc act gac aga gtt	576
Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val	
180 185 190	
gtt ctt att gga gga aaa ccc gat agg gtt gta gag tgc ata aag atc	624
Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile	
195 200 205	
atc ctt gat ctt ata tct gag tct ccc atc aaa gga cgt gca cag cct	672
Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro	
210 215 220	
tat gat ccc aat ttt tac gat gaa acc tat gat tat ggt ggt ttt aca	720
Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr	
225 230 235 240	
atg atg ttt gat gac cgt cgc gga cgc cca gtg gga ttt ccc atg cgg	768
Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg	
245 250 255	

gga aga ggt ggt ttt gac aga atg cct cct ggt cgg ggt ggg cgt ccc	816
Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro	
260 265 270	
atg cct cca tct aga aga gat tat gat gat atg agc cct cgt cga gga	864
Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly	
275 280 285	
cca cct ccc cct cct ccc gga cga ggc ggc cgg ggt ggt agc aga gct	912
Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala	
290 295 300	
cgg aat ctt cct ctt cct cca cca cca cca cct aga ggg gga gac ctc	960
Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu	
305 310 315 320	
atg gcc tat gac aga aga ggg aga cct gga gac cgt tac gac ggc atg	1008
Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met	
325 330 335	
gtt ggt ttc agt gct gat gaa act tgg gac tct gca ata gat aca tgg	1056
Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp	
340 345 350	
agc cca tca gaa tgg cag atg gct tat gaa cca cag ggt ggc tcc gga	1104
Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly	
355 360 365	
tat gat tat tcc tat gca ggg ggt cgt ggc tca tat ggt gat ctt ggt	1152
Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly	
370 375 380	
gga cct att att act aca caa gta act att ccc aaa gat ttg gct gga	1200
Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly	
385 390 395 400	
tct att att ggc aaa ggt ggt cag cgg att aaa caa atc cgt cat gag	1248
Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu	
405 410 415	
tcg gga gct tcg atc aaa att gat gag cct tta gaa gga tcc gaa gat	1296
Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp	
420 425 430	
cgg atc att acc att aca gga aca cag gac cag ata cag aat gca cag	1344
Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln	
435 440 445	
tat ttg ctg cag aac agt gtg aag cag tat gca gat gtt gaa gga ttc	1392
Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ala Asp Val Glu Gly Phe	
450 455 460	
taa	1395

<210> 104
 <211> 464
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
 1 5 10 15
 Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
 20 25 30
 Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
 35 40 45
 Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
 50 55 60
 Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp
 65 70 75 80
 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
 85 90 95
 Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
 100 105 110
 Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
 115 120 125
 Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
 130 135 140
 Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
 145 150 155 160
 Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
 165 170 175
 Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
 180 185 190
 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
 195 200 205
 Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
 210 215 220
 Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
 225 230 235 240
 Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
 245 250 255
 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
 260 265 270

Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
 275 280 285

Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
 290 295 300

Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
 305 310 315 320

Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
 325 330 335

Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
 340 345 350

Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
 355 360 365

Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
 370 375 380

Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
 385 390 395 400

Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
 405 410 415

Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
 420 425 430

Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
 435 440 445

Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ala Asp Val Glu Gly Phe
 450 455 460

<210> 105

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic probe

<400> 105

agactgtgtg tttactgcgt gggaggag

28

<210> 106

<211> 101

<212> DNA

<213> Hepatitis B virus

<400> 106

ggcatacttc aaagactggt tgtttaatga ctgggaggag ttggggagg agattagatt 60

aaaggtcttt gtattaggag gctgtaggca taaattggc t

101

<210> 107

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 107

Asp Leu Ala Gly Ser Ile Ile Gly Lys

1

5

<210> 108

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 108

Gly Gly Asp Leu Met Ala Tyr Asp Arg

1

5

<210> 109

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 109

Val Val Leu Ile Gly Gly Lys Pro Asp Arg

1

5

10

<210> 110

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 110

Gly Ser Asp Phe Asp Cys Glu Leu Arg

1

5

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<210> 111
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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```
<400> 111
Asn Thr Asp Glu Met Val Glu Leu Arg
  1                      5
```

```
<210> 112
<211> 10
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic peptide

```
<400> 112
Gly Gly Asp Leu Met Ala Tyr Asp Arg Arg
  1             5             10
```

```
<210> 113
<211> 10
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
```

<400> 113
Gly Gly Asp Leu Met Ala Tyr Asp Arg Arg
1 5 10

```
<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
```

```
<400> 114
Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg
  1             5             10
```

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 115
Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg
1 5 10

<210> 116
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 116
Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg
1 5 10

<210> 117
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 117
Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp Arg
1 5 10

<210> 118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 118
Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys
1 5 10

<210> 119

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 119

Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg
1 5 10

<210> 120

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 120

Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile Gly Val Lys
1 5 10 15

<210> 121

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 121

Ile Ile Pro Thr Leu Glu Glu Tyr Gln His Tyr Lys
1 5 10

<210> 122

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 122

Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg
1 5 10

<210> 123
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 123
 Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg
 1 5 10

<210> 124
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 124
 Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala Phe Lys Arg
 1 5 10

<210> 125
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 125
 Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp Ser Ser Gly Pro Glu
 1 5 10 15

Arg

<210> 126
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 126
 Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp Ser Ser Gly Pro Glu
 1 5 10 15

Arg

<210> 127

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 127

Ala	Leu	Arg	Thr	Asp	Tyr	Asn	Ala	Ser	Val	Ser	Val	Pro	Asp	Ser	Ser
1				5					10					15	

Gly

<210> 128

<211> 460

<212> PRT

<213> Homo sapiens

<400> 128

Met	Glu	Thr	Glu	Gln	Pro	Glu	Glu	Thr	Phe	Pro	Asn	Thr	Glu	Thr	Asn
1				5					10					15	

Gly	Glu	Phe	Gly	Lys	Arg	Pro	Ala	Glu	Asp	Met	Glu	Glu	Glu	Gln	Ala
			20					25						30	

Phe	Lys	Arg	Ser	Arg	Asn	Thr	Asp	Glu	Met	Val	Glu	Leu	Arg	Ile	Leu
		35					40					45			

Leu	Gln	Ser	Lys	Asn	Ala	Gly	Ala	Val	Ile	Gly	Lys	Gly	Gly	Lys	Asn
	50					55					60				

Ile	Lys	Ala	Leu	Arg	Thr	Asp	Tyr	Asn	Ala	Ser	Val	Ser	Val	Pro	Asp
65					70					75				80	

Ser	Ser	Gly	Pro	Glu	Arg	Ile	Leu	Ser	Ile	Ser	Ala	Asp	Ile	Glu	Thr
				85					90					95	

Ile	Gly	Glu	Ile	Leu	Lys	Lys	Ile	Ile	Pro	Thr	Leu	Glu	Glu	Gly	Leu
			100					105						110	

Gln	Leu	Pro	Ser	Pro	Thr	Ala	Thr	Ser	Gln	Leu	Pro	Leu	Glu	Ser	Asp
		115					120					125			

Ala	Val	Glu	Cys	Leu	Asn	Tyr	Gln	His	Tyr	Lys	Gly	Ser	Asp	Phe	Asp
	130					135					140				

Cys	Glu	Leu	Arg	Leu	Leu	Ile	His	Gln	Ser	Leu	Ala	Gly	Gly	Ile	Ile
145					150					155					160

Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
 165 170 175
 Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
 180 185 190
 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
 195 200 205
 Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
 210 215 220
 Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
 225 230 235 240
 Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
 245 250 255
 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
 260 265 270
 Met Pro Pro Ser Arg Arg Asp Asp Tyr Asp Asp Met Ser Pro Arg Arg
 275 280 285
 Gly Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Ser Arg Ala Arg Asn
 290 295 300
 Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu Met Ala
 305 310 315 320
 Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met Val Gly
 325 330 335
 Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp Ser Pro
 340 345 350
 Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly Tyr Asp
 355 360 365
 Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly Gly Pro
 370 375 380
 Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly Ser Ile
 385 390 395 400
 Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu Gly Ala
 405 410 415
 Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp Arg Ile Ile
 420 425 430
 Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln Tyr Leu Leu
 435 440 445
 Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
 450 455 460

<210> 129
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
 1 5 10 15
 Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
 20 25 30
 Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
 35 40 45
 Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
 50 55 60
 Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp
 65 70 75 80
 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
 85 90 95
 Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
 100 105 110
 Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
 115 120 125
 Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
 130 135 140
 Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
 145 150 155 160
 Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
 165 170 175
 Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
 180 185 190
 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
 195 200 205
 Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
 210 215 220
 Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
 225 230 235 240
 Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
 245 250 255
 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
 260 265 270

Met Pro Pro Ser Arg Arg Asp Asp Tyr Asp Asp Met Ser Pro Arg Arg
 275 280 285

Gly Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Ser Arg Ala Arg Asn
 290 295 300

Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu Met Ala
 305 310 315 320

Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met Val Gly
 325 330 335

Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp Ser Pro
 340 345 350

Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly Tyr Asp
 355 360 365

Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly Gly Pro
 370 375 380

Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly Ser Ile
 385 390 395 400

Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu Gly Ala
 405 410 415

Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp Arg Ile Ile
 420 425 430

Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln Tyr Leu Leu
 435 440 445

Gln Asn Ser Val Lys Gln Tyr Ala Asp Val Glu Gly Phe
 450 455 460

<210> 130

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 130

Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala Phe Lys Arg Ser Arg
 1 5 10 15

Asn Thr Asp Glu Met Val Glu Leu Arg
 20 25

<210> 131

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 131

Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp Ser Ser
 1 5 10 15

Gly

<210> 132

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 132

Gly Ser Asp Phe Asp Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu
 1 5 10 15

Ala Gly Gly Ile Ile Gly Val Lys
 20

<210> 133

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 133

Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val Val Leu Ile
 1 5 10 15

Gly Gly Lys Pro Asp Arg
 20

<210> 134

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 134

Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg
1 5 10

<210> 135

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 135

Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu Met
1 5 10 15

Ala Tyr Asp Arg Arg
20

<210> 136

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 136

Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp Arg
1 5 10